



IFWO

## RAW SEQUENCE LISTING

DATE: 09/17/2004

PATENT APPLICATION: US/10/829,388

TIME: 12:09:17

Input Set : A:\41133006.app

Output Set: N:\CRF4\09172004\J829388.raw

3 <110> APPLICANT: ROSSI, EDMUND A.  
 4     CHANG, CHIEN HSING  
 5     MCBRIDE, WILLIAM J.  
 7 <120> TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX  
 9 <130> FILE REFERENCE: 41133-0006US1  
 11 <140> CURRENT APPLICATION NUMBER: 10/829,388  
 12 <141> CURRENT FILING DATE: 2004-04-22  
 14 <150> PRIOR APPLICATION NUMBER: 60/464,532  
 15 <151> PRIOR FILING DATE: 2003-04-22  
 17 <150> PRIOR APPLICATION NUMBER: 60/525,391  
 18 <151> PRIOR FILING DATE: 2003-11-24  
 20 <160> NUMBER OF SEQ ID NOS: 20  
 22 <170> SOFTWARE: PatentIn version 3.2  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 370  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Artificial Sequence  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Chimeric sequence from multiple species  
 32 <400> SEQUENCE: 1  
 33 Glu Ala Glu Ala Glu Phe Met Glu Val Gln Leu Val Glu Ser Gly Gly  
 34 1                                 5                                 10                                 15  
 37 Asp Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser  
 38                                 20                                 25                                 30  
 41 Gly Phe Thr Phe Ser Ile Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro  
 42                                 35                                 40                                 45  
 45 Gly Lys Gly Leu Glu Trp Val Ala Thr Leu Ser Gly Asp Gly Asp Asp  
 46                                 50                                 55                                 60  
 49 Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp  
 50 65                                 70                                 75                                 80  
 53 Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu  
 54                                 85                                 90                                 95  
 57 Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Val Arg Leu Gly Asp Trp Asp  
 58                                 100                                 105                                 110  
 61 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser Gly Gly  
 62                                 115                                 120                                 125  
 65 Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala  
 66                                 130                                 135                                 140  
 69 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val  
 70 145                                 150                                 155                                 160  
 73 Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
 74                                 165                                 170                                 175  
 77 Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg

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78          180          185          190
81 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
82          195          200          205
85 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
86          210          215          220
89 Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Leu Glu
90 225          230          235          240
93 Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
94          245          250          255
97 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp
98          260          265          270
101 Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
102          275          280          285
105 Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr
106          290          295          300
109 Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
110 305          310          315          320
113 Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
114          325          330          335
117 Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr
118          340          345          350
121 Trp Gly Gln Gly Thr Pro Val Thr Val Ser Val Asp His His His His
122          355          360          365
125 His His
126          370
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 363
131 <212> TYPE: PRT
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Chimeric sequence from multiple species
137 <400> SEQUENCE: 2
138 Glu Ala Glu Ala Glu Phe Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser
139 1          5          10          15
142 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
143          20          25          30
146 Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
147          35          40          45
150 Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val
151          50          55          60
154 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
155 65          70          75          80
158 Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
159          85          90          95
162 Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
163          100          105          110
166 Arg Gly Gly Gly Gln Phe Met Glu Val Gln Leu Val Glu Ser Gly Gly
167          115          120          125
170 Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser

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171      130      135      140
174 Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro
175 145      150      155      160
178 Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr
179      165      170      175
182 Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp
183      180      185      190
186 Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu
187      195      200      205
190 Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp
191      210      215      220
194 Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Gly Gly Gly
195 225      230      235      240
198 Gly Ser Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser
199      245      250      255
202 Pro Gly Glu Arg Val Thr Leu Thr Cys Lys Ser Ser Gln Ser Leu Phe
203      260      265      270
206 Asn Ser Arg Thr Arg Lys Asn Tyr Leu Gly Trp Tyr Gln Gln Lys Pro
207      275      280      285
210 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser
211      290      295      300
214 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
215 305      310      315      320
218 Leu Thr Ile Asn Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
219      325      330      335
222 Thr Gln Val Tyr Tyr Leu Cys Thr Phe Gly Ala Gly Thr Lys Leu Glu
223      340      345      350
226 Leu Lys Arg Leu Asp His His His His His His
227      355      360

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230 &lt;210&gt; SEQ ID NO: 3

231 &lt;211&gt; LENGTH: 26

232 &lt;212&gt; TYPE: DNA

233 &lt;213&gt; ORGANISM: Artificial Sequence

235 &lt;220&gt; FEATURE:

236 &lt;223&gt; OTHER INFORMATION: Synthesized Oligonucleotide

238 &lt;400&gt; SEQUENCE: 3

239 gatccctgc agggagctca ctagta

26

242 &lt;210&gt; SEQ ID NO: 4

243 &lt;211&gt; LENGTH: 26

244 &lt;212&gt; TYPE: DNA

245 &lt;213&gt; ORGANISM: Artificial Sequence

247 &lt;220&gt; FEATURE:

248 &lt;223&gt; OTHER INFORMATION: Synthesized oligonucleotide

250 &lt;400&gt; SEQUENCE: 4

251 gatccctgc agggagctca ctagta

26

254 &lt;210&gt; SEQ ID NO: 5

255 &lt;211&gt; LENGTH: 43

256 &lt;212&gt; TYPE: DNA

257 &lt;213&gt; ORGANISM: Artificial Sequence

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259 <220> FEATURE:
260 <223> OTHER INFORMATION: Synthesized oligonucleotide
262 <400> SEQUENCE: 5
263 catactcgag ggcggaggta gcgaggtcca actggtggag agc 43
266 <210> SEQ ID NO: 6
267 <211> LENGTH: 29
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Synthesized oligonucleotide
274 <400> SEQUENCE: 6
275 cttagtcgac ggagacggtg accgggggtc 29
278 <210> SEQ ID NO: 7
279 <211> LENGTH: 30
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Synthesized oligonucleotide
286 <400> SEQUENCE: 7
287 ctaggaattc gacatccagc tgacccagag 30
290 <210> SEQ ID NO: 8
291 <211> LENGTH: 39
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: Synthesized oligonucleotide
298 <400> SEQUENCE: 8
299 cgtacaattg gccacctcca cgtttgattt ccaccttgg 39
302 <210> SEQ ID NO: 9
303 <211> LENGTH: 1110
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Chimeric sequence from multiple organisms
310 <400> SEQUENCE: 9
311 gaggtgaag ctgaattcat ggaagtgcag ctggtggagt cagggggaga cttagtgaag 60
313 cctggagggg ccctgaaact ctctgtgca gcctctggat tcactttcag tatttacacc 120
315 atgtcttggc ttcgccagac tccgggaaag gggctggagt gggctcgcaac cctgagtggg 180
317 gatggtgatg acatctacta tccagacagt gtgaagggtc gattcaccat ctccagagac 240
319 aatgccaaga acagcctata tctgcagatg aacagtctaa gggctgagga cacggccttg 300
321 tattactgtg caagggtgcg acttggggac tgggacttcg atgtctgggg ccaaggggacc 360
323 acggtctccg tctctcagg aggtggcgga tccgacatcc agctgacca gagcccaagc 420
325 agcctgagcg ccagcgtggg tgacagagtg accatcacct gtaaggccag tcaggatgtg 480
327 ggtacttctg tagcttggtg ccagcagaag ccaggtaagg ctccaaagct gctgatctac 540
329 tggacatcca cccggcacac tgggtgtgcca agcagattca gcggtagcgg tagcgttacc 600
331 gacttcacct tcaccatcag cagcctccag ccagaggaca tcgccacct ctactgccag 660
333 caatatagcc tctatcggtc gttcggccaa gggaccaagg tggaaatcaa acgtctcgag 720
335 ggcggaggta gcgaggtcca actggtggag agcgggtggag gtgttggtgca acctggccgg 780
337 tccctgcgcc tgtcctgctc cgcactctggc ttcgatttca ccacatattg gatgagttgg 840

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339 gtgagacagg cacctggaaa aggtcttgag tggattggag aaattcatcc agatagcagt 900
341 acgattaact atgcgcgcgtc tctaaaggat agatttacia tatcgcgaga caacgccaaag 960
343 aacacattgt tcctgcaaat ggacagcctg agaccgaag acaccggggt ctatttttgt 1020
345 gcaagccttt acttcggctt cccctgggtt gcttattggg gccaaaggac cccggtcacc 1080
347 gtctccgtcg accatcatca tcatcatcat 1110

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350 &lt;210&gt; SEQ ID NO: 10

351 &lt;211&gt; LENGTH: 1089

352 &lt;212&gt; TYPE: DNA

353 &lt;213&gt; ORGANISM: Artificial Sequence

355 &lt;220&gt; FEATURE:

356 &lt;223&gt; OTHER INFORMATION: Chimeric sequence from multiple organisms

358 &lt;400&gt; SEQUENCE: 10

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359 gaggtgaag ctgaattcga catccagctg acccagagcc caagcagcct ggcgcgcagg 60
361 gtgggtgaca gagtgaccat cacctgtaag gccagtcagg atgtgggtac ttctgtagct 120
363 tggtagcagc agaagccagg taaggctcca aagctgctga tctactggac atccaccgag 180
365 cactactggtg tgccaagcag attcagcggg agcggtagcg gtaccgactt caccttcacc 240
367 atcagcagcc tccagccaga ggacatcgcc acctactact gccagcaata tagcctctat 300
369 cggtcggttcg gccaaaggac caaggtggaa atcaaactg gaggtggcca attcatggag 360
371 gtccaactgg tggagagcgg tggaggtgtt gtgcaactg gccgggtcct gcgcctgtcc 420
373 tgctccgcat ctggcttcga tttcaccaca tattggatga gttgggtgag acaggcacct 480
375 ggaaaagggtc ttgagtggat tggagaaatt catccagata gcagtacgat taactatgcg 540
377 ccgtctctaa aggatagatt tacaatatcg cgagacaacg ccaagaacac attgttctcg 600
379 caaatggaca gcctgagacc cgaagacacc ggggtctatt tttgtgcaag cctttacttc 660
381 ggcttcccct gggtttgctta ttggggccaa gggaccgagg tcaccgtctc cggaggcggg 720
383 ggatccgaca ttgtgatgac acaatctcca tctcctctgg ctgtgtcacc cggggagagg 780
385 gtcactctga cctgcaaatc cagtcagagt ctgttcaaca gtagaaccgg aaagaactac 840
387 ttgggttggt accagcagaa accagggcag tctcctaaac ttctgatcta ctgggcactc 900
389 actcgggaat ctgggggtccc tgatcgcttc tcaggcagtg gatccggaac agatttcact 960
391 ctcaccatca acagtctgca ggctgaagac gtggcagttt attactgcac tcaagtttat 1020
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395 catcatcat 1089

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398 &lt;210&gt; SEQ ID NO: 11

399 &lt;211&gt; LENGTH: 364

400 &lt;212&gt; TYPE: PRT

401 &lt;213&gt; ORGANISM: Artificial Sequence

403 &lt;220&gt; FEATURE:

404 &lt;223&gt; OTHER INFORMATION: Chimeric sequence from multiple species

406 &lt;400&gt; SEQUENCE: 11

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407 Met Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly
408 1 5 10 15
411 Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ile
412 20 25 30
415 Tyr Thr Met Ser Trp Leu Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
416 35 40 45
419 Val Ala Thr Leu Ser Gly Asp Gly Asp Asp Ile Tyr Tyr Pro Asp Ser
420 50 55 60
423 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
424 65 70 75 80
427 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr

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**VERIFICATION SUMMARY**

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